

GAATCCCCCAACAGAGCCAGCTCTCCATCTAGTGGACAGGAAGCTAGCAGCAAAACC	39 (UPPER: SEQ ID NO.: 1) 19 (LOWER: SEQ ID NO.: 4)
TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAGAGAGTTAATTCATGTAGACAT	119 39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTTCATGGAGGGCAAC	179 59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTATTATGACAGGGTGGAAACAAG	239 79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC M D Y Q V S S P I Y D I N Y Y T S E P C	299 99

FIG. 1A-1

CAAAAATCAATGTGAAGCAAAATCGAGCCCGCCTCCTGCTCCGCTCTACTCACTGGTG	359
Q K I N V K Q I A A R L L P P L Y S L V	119
TTCAATCTTTGGTTTGTGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG	419
F I F G F V G N M L V I L I L I N C K R	139
CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479
L K S M T D I Y L L N L A I S D L F F L	159
CTTACTGTCCCCTTCTGGGCTCACTAIGCTGCCGCCAGTGGGACTTTGGAAATACAATG	539
L T V P F W A H Y A A A Q W D F G N T M	179
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTCTCGGAATCTTCTTCATCATC	599
C Q L L T G L Y F I G F F S G I F F I I	199
CTCCTGACAAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAGCCAGG	659
L L T I D R Y L A V V H A V F A L K A R	219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGGCTCT	719
T V T F G V V T S V I T W V V A V F A S	239
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGTCTTCATTACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259

CATTTTCCATACA
H F P Y

FIG. 1A-2

59 (UPPER: SEQ ID NO.: 2)
19 (LOWER: SEQ ID NO.: 5)

GAATTCCTCCCAACAGAGCCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAAACC

TTCCCTTCACTACAAAACCTTCATGTCTTGGCCAAAAGAGAGTTAATTCAATGTAGACAT 119
39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCAATTCATGGAGGGCAAC 179
59

TAAATACATTCTAGGACTTTATAAAAGATCACITTTTATTATGCACAGGGTGAACAAG 239
79

ATGGATTATCAAGTGCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC 299
M D Y Q V S S P I Y D I N Y Y T S E P C 99

FIG. 1B-1

CAAAAATCAATGTGAAGCAAATCGCAGCCCGCTCCTGCCTCCGCTCTACTCACTGGTG	359
Q K I N V K Q I A A R L L P P L Y S L V	119
TTCACTCTTTGGTTTGTGGGCAACATGCTGGTCATCCTCATGATAAACTGCAAAAGG	419
F I F G F V G N M L V I L I L I N C K R	139
CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTT	479
L K S M T D I Y L L N L A I S D L F F L	159
CTTACTGTCCCTTCTGGGCTCACTATGCTGCGGCCAGTGGGACTTTGGAAATACAATG	539
L T V P F W A H Y A A A Q W D F G N T M	179
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTCTCTGGAATCTTCTTCATCATC	599
C Q L L T G L Y F I G F F S G I F F I I	199
CTCCTGACAAATCGATAGGTACCTGGCTGTGTCATGCTGTGTTTGCTTTAAAGCCAGG	659
L L T I D R Y L A V V H A V F A L K A R	219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGTGGTGGCTGTGTTGCGTCT	719
T V T F G V V T S V I T W V V A V F A S	239
CTCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGTCTTCATTACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259
CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCAGACATTAAAGATAGTCATC	839
H F P Y S Q Y Q F W K N F Q T L K I V I	279

FIG. 1B-2

TTGGGGCTGCTCCGCTGCTGTGTCATGGTCATCTGCTACTCGGGAATCCTAAAACT	899
L G L V L P L L V M V I C Y S G I L K T	299
CTGCTTCGGTGTGGAATGAGAAGAGGACAGGGCTGTGAGGCTTATCTTCACCATC	959
L L R C R N E K K R H R A V R L I F T I	319
ATGATTGTTTATTTCTCTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTTC	1019
M I V Y F L F W A P Y N I V L L L N T F	339
CAGGAATCTTTGGCCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAG	1079
Q E F F G L N N C S S S N R L D Q A M Q	359
GTGACAGAGACTCTTGGGATGACGCACCTGCTGCATCAACCCCATCATCTATGCCTTTGTC	1139
V T E T L G M T H C C I N P I I Y A F V	379
GGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTTC	1199
G E K F R N Y L L V F F Q K H I A K R F	399
TGCAAAATGCTGTTCTATTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC	1259
C K C C S I F Q Q E A P E R A S S V Y T	419
CGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACACGGACTCAAGTGGGCTGGT	1319
R S T G E Q E I S V G L *	439
GACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTCATACACAGCCTGGGCTGGGGTNGG	1379
	459
TTGGNNGAGGTCTTTTAAAGGAAGTTACTGTATTAGAGGGTCTAAGATTTCATCCATT	1439
	479
TATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC	

FIG. 1B-3

GAATTC	59 (UPPER: SEQ ID NO. 3)
CCCCCAACAGAGCCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAC	19 (LOWER: SEQ ID NO. 6)
TTCCCTTCACTACAAACTTCATTGCTTGGCCAAAAGAGAGTTAATTC	119
AAATGTAGACAT	39
CTATGTAGGCAATTAAAAACCTATTGTATGTATAAACAGTTTGCCATTCATGGAGGGCAAC	179
	59
TAAATACATTCTAGGACTTTATAAAGATCACTTTTATTATGCAAGGGTGAACAAG	239
	79
ATGGATTATCAAGTGTCAAGTCCAAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99

FIG. 1D-1

CAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	359
Q K I N V K Q I A A R L L P P L Y S L V	119
TTCAATCTTTGGTTTGTGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG	419
F I F G F V G N M L V I L I L I N C K R	139
CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479
L K S M T D I Y L L N L A I S D L F F L	159
CTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG	539
L T V P F W A H Y A A A Q W D F G N T M	179
TGTCAACTCTTGACAGGGCTCTATTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599
C Q L L T G L Y F I G F F S G I F I I	199
CTCCTGACAATCGATAGGTACCTGGCTGTCTCGTCCATGCTGTGTTTGCTTTAAAGCCAGG	659
L L T I D R Y L A V V H A V F A L K A R	219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTGCGTCT	719
T V T F G V V T S V I T W V V A V F A S	239
CTCCAGGAATCATCTTTACCAGATCTCAAAAAGAGGTCTTCAATACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259
CATTTTCCATACATTAAAGATAGTCATCTTGGGGCTGGTCCCTGCCGCTGCTTGTCAATGGT	839
H F P Y I K D S H L G A G P A A C H G	279

FIG. 1D-2

CATCTGCTACTCGGGAATCCTAAAACTCTGCTTCGGTGTGCGAAATGAGAAAGAGGCA	899
H L L L G N P K N S A S V S K *	299
CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTCTCGGGCTCCCTA	959
	319
CAACATTGTCTCTCTGAAACACCTTCCAGGAATCTTTGGCCCTGAATAATTGCAGTAG	1019
	339
CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACCTGCTG	1079
	359
CATCAACCCCATCATCTATGCTTGTCTGGGAGAAAGTTCAGAAACTACCTCTTAGTCTT	1139
	379
CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAAATGCTGTCTTATTTTCCAGCAAGAGGC	1199
	399
TCCCAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG	1259
	419
CTTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT	1319
	439
TTCATACACAGCCTGGGCTGGGGGTNGGTTGGNNGAGGTCTTTTAAAGGAAGTTACT	1379
	459
GTTATAGAGGGTCTAAGATTTCATCCATTTATTTTGGCATCTGTTTAAAGTAGATTAGATCC	1439
	479

GAATTC

FIG. 1D-3

		I		II					
CCR5	1	MDYQVSSP	YDINYYTSEPCQKUNVKQIA	ARLLPPLYSLSVFI	FGVGNMLVILILINCKRLKSM	TDIYLLNLAISD	LEFLIT	83	
hCC-R2b	6	MLSTSRSRFIRNTN	ESGEEVTTFFDYDYCAPCHKFTD	VKQIGACQLLPPLYSLSVFI	FGVGNMLVILILINCKRLK	CTDDIYLLNLAISD	LEFLIT	95	
hCC-R3		MTTSLD	TVETFGTTSYDDVGLLQEKADTRALMA	QFVPPPLYSLSVFTV	GLIGNVWVWMLIKYRRIR	IMTNIIYLLNLAISD	LEFLIT	87	
hCC-R1		METPNT	EDYDTTTEFDYGDATPCQKMN	ERAFGAQLLPPLYSLSVFI	GLVGNMLVWVILNQKRLK	MNTSIYLLNLAISD	LEFLIT	87	
hCC-R4		MNPTD	IADTTILDESISY	SNLYESIPKPTNEGKAFGELEFL	PPLYSLSVFI	FGVGNMLVILILINCKRLK	SMTDVYLLNLAISD	LEFLIT	92
		III		IV					
CCR5		VPFWAHYA	ARQMDFGNIMCQLLTGLYFTGFFSGIFFIILLTIDRYLA	WHA	VPFALKARTVTFGVVTSVITW	WAVPASLPGIIF	TRSQKEG	177	
hCC-R2b		LPFWAHYA	ANENWFGNIMCKLFTGLYHIGVFGGIFFIILLTIDRYLA	WHA	VPFALKARTVTFGVVTSVITW	WAVPASLPGIIF	TRSQKEG	189	
hCC-R3		LPFWAHYA	VRGHNWFGNIMCKLFTGLYHIGVFGGIFFIILLTIDRYLA	WHA	VPFALKARTVTFGVVTSVITW	WAVPASLPGIIF	TRSQKEG	182	
hCC-R1		LPFWAHYA	KLDWFGNIMCKLFTGLYHIGVFGGIFFIILLTIDRYLA	WHA	VPFALKARTVTFGVVTSVITW	WAVPASLPGIIF	TRSQKEG	182	
hCC-R4		LPFWAHYA	ADQWFGNIMCKLFTGLYHIGVFGGIFFIILLTIDRYLA	WHA	VPFALKARTVTFGVVTSVITW	WAVPASLPGIIF	TRSQKEG	186	

FIG. 2A

CCR5
 hcc-R2b
 hcc-R3
 hcc-R1
 hcc-R4

VI

V

YTCSSHPFYSQYQFWKNFOTLKIVILGLVPLLVVICYSGLKTLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLNTFQEFFGLNNG 272
 WCGPYFPRG...WNNFHTIMRNILGLVPLLVVICYSGLKTLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLNTFQEFFGLSNC 280
 TLCSALYPEDTVYSNRHHTTIRMTTFCLVPLLVMAICVIGITKTLRCRNEKKKYLKARLIEIVIMAVFRLFWAPYNIVALLSSYQSILFGNDQ 276
 HTCSLHFPHESLREWKLFQALKLNLFGVPLLVMIICVIGITKTLRCRNEKKSKAVRLIEIVIMIIFFLEWTPYNLTILISVFQDELFTHEC 276
 TYCKTKYSLSNST.TWKVLSSEINILGLVPLLVVICYSGLKTLRCRNEKKKYLKARLIEIVIMIIFFLEWTPYNIVLLNTFQEFFGLNNG 279

CCR5
 hcc-R2b
 hcc-R3
 hcc-R1
 hcc-R4

VII

SSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNVLVFFQKHTAKR.FCKCCSIFQCEAFERASSVYTRSTGEQETISVGL 352
 ESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRNVLVFFQKHTAKR.FCKCCSIFQCEAFERASSVYTRSTGEQETISVGL 360
 ERSKHLDMVMTVEVIAYSHCCNPNIIYAFVGERFRNVLVFFQKHTAKR.LCRYIPFLPSEKILERTSSV.SPSTAEPLSIVF 355
 EQSRHLDLAWQVTEVIAYTHCCNPNIIYAFVGERFRNVLVFFQKHTAKR.LVMWLPFLSVDRLEKIVSSV.SPSTGEHETISVGL 355
 TTERYLQVATQATETLAFVHCCINPNIIYAFVGEKFRNVLVFFQKHTAKR.LVMWLPFLSVDRLEKIVSSV.SPSTGEHETISVGL 360

FIG. 2B

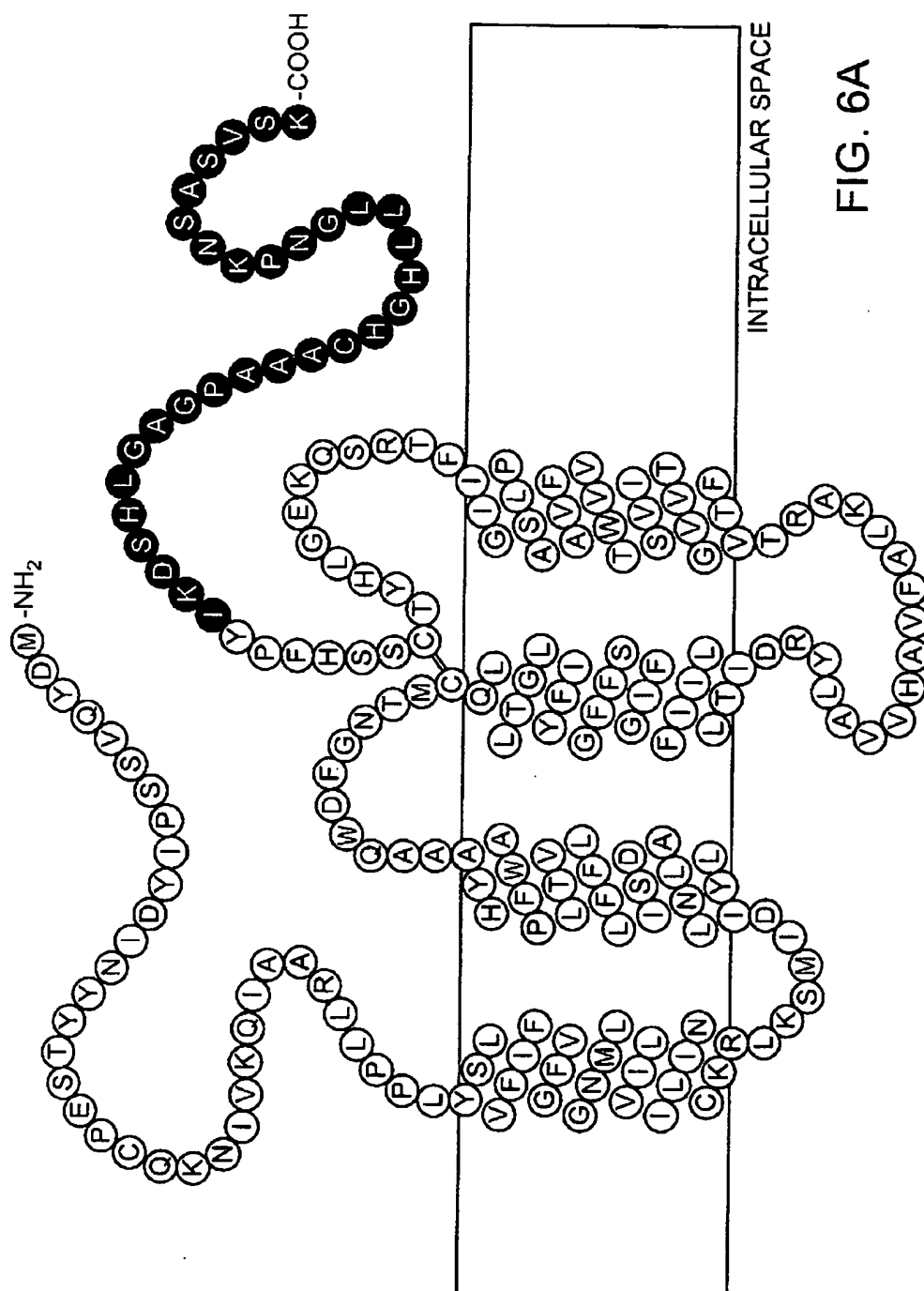


FIG. 6B